



1 GTCCCTCCACCATGCACTCGCTGGGCTTCTTCTGTGTGGCGTGTTCTCTGTCTCGCCGCTG  
-----+-----+-----+-----+-----+-----+-----+-----+  
CAGGAAGGTGCTACGTGAGCGACCCGAAGAAGAGACACCGCACAAAGAGACGAGCGGCGAC  
M H S L G F F S V A C S L L A A A  
60  
61 CGCTGCTCCCGGTCCTCGCGAGGCGCCCGCGCGCGCGCTTCGAGTCCGGACTCG  
-----+-----+-----+-----+-----+-----+-----+-----+  
GCGACGAGGGCCAGGAGCGCTCCGGGGCGGGCGGGGGAAGCTCAGGCCTGAGC  
L L P G P R E A P A A A A A F E S G L D  
120  
121 ACCTCTCGGACGCGGAGCCCGACGGGGCGAGGCCACGGCTTATGCAAGCAAAGATCTGG  
-----+-----+-----+-----+-----+-----+-----+-----+  
TGGAGAGCCTCGGCCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCTGTCTTAGACC  
L S D A E P D A G E A T A Y A S K D L E  
180  
181 AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACCTCATGACTGTACTCTACCCAGAAT  
-----+-----+-----+-----+-----+-----+-----+-----+  
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGTCTTA  
E Q L R S V S S V D E L M T V L Y P E Y  
240  
241 ATTGGAAAATGTACAAAGTGTGCTAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG  
-----+-----+-----+-----+-----+-----+-----+-----+  
TAACCTTTTACATGTTACAGTCGATTCTTCTCCGACCGTGTGTAATGCTCTTGTCC  
W K M Y K C Q L R K G G W Q H N R E Q A  
300  
301 CCAACCTCAACTCAAGGACAGAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG  
-----+-----+-----+-----+-----+-----+-----+-----+  
GGTTGGAGTTGAGTTCCTGTCTTCTCTGATAATTTAAACGACGTCGTGTAATATTATGTC  
N L N S R T E E T I K F A A A H Y N T E  
360

FIG. 1A



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361 AGATCTTGAAAAGTATTGATAAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT  
-----+-----+-----+-----+-----+-----+-----+  
TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA  
I L K S I D N E W R K T Q C M P R E V C  
420

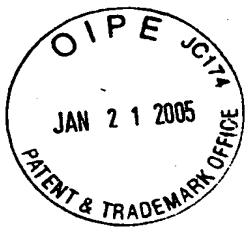
421 GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG  
-----+-----+-----+-----+-----+-----+-----+  
CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTGTGGAAGAAATTTGGAGGTACAC  
I D V G K E F G V A T N T F F K P P C V  
480

481 TGTCCGCTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA  
-----+-----+-----+-----+-----+-----+-----+  
ACAGGCAGATGTCTACACCCCAACGACGTTATCATTCCCGACGTCACGTACTTGTGGT  
S V Y R C G G C C N S E G L Q C M N T S  
540

541 GCACGAGCTACCTCAGCAAGACGTTATTGAAATTACAGTGCCCTCTCTCTCAAGGCCCA  
-----+-----+-----+-----+-----+-----+-----+  
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTACGGAGAGAGAGTCCCGGGT  
T S Y L S K T L F E I T V P L S Q G P K  
600

601 AACCAGTAACAATCAGTTTTGCCCAATCACACTTCTCTGCCGATGCATGTCTAAACTGGATG  
-----+-----+-----+-----+-----+-----+-----+  
TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC  
P V T I S F A N H T S C R C M S K L D V  
660

FIG. 1B



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661 TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC  
720 -----+-----+-----+-----+-----+-----+-----+  
AAATGCTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG  
Y R Q V H S I I R R S L P A T L P Q C Q  
780 AGCAGCGAACAAGACCTGCCCCCACCACCAATTACATGTGGAATAATCACATCTGCAGATGCC  
-----+-----+-----+-----+-----+-----+-----+  
TCCGTCGCTTGTCTCGACGGGGTGGTTAAATGTACACCTTATTAGTGTAGACGTTCTACGG  
A A N K T C P T N Y M W N N H I C R C L  
840 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC  
-----+-----+-----+-----+-----+-----+-----+  
ACCGAGTCCTTCTAAATAACAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG  
A Q E D F M F S S D A G D D S T D G F H  
900 ATGACATCTGTGGACCAACAAGAGCTGGATGAAGAGACCTGTCAAGTGTGTCTGCAGAG  
-----+-----+-----+-----+-----+-----+-----+  
TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC  
D I C G P N K E L D E E T C Q C V C R A  
960 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCCACAAGAACTAGACAGAAACTCATGCCAGT  
-----+-----+-----+-----+-----+-----+-----+  
GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA  
G L R P A S C G P H K E L D R N S C Q C

FIG. 1C



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961	GTGTCGTAAACAACTCTCCCAAGCAATGTGGGCCAACCGAGAATTGATGAAA -----+-----+-----+-----+-----+-----+-----+ CACAGACATTTTGTGAGAGGGGTGCGTTACACCCCGTTGGCTCTTAAACTACTTT V C K N K L F P S Q C G A N R E F D E N	1020
1021	ACACATGCCAGTGTATGTAAAGAACCTGCCCCAGAAAATCAACCCCTAAATCCTGGAA -----+-----+-----+-----+-----+-----+-----+ TGTGTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGATTTAGGACCTT T C Q C V C K R T C P R N Q P L N P G K	1080
1081	AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC -----+-----+-----+-----+-----+-----+-----+ TTACACGGACACTTACATGTCTTTCAGGTGCTTTACGAACAATTTTCCTTTCTTCAAGG C A C E C T E S P Q K C L L K G K K F H	1140
1141	ACCACCAACATGCAGCTGTTACAGACGGCCCATGTACGAACCCGACAGGCTTGTGAGC -----+-----+-----+-----+-----+-----+-----+ TGGTGGTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG H Q T C S C Y R R P C T N R Q K A C E P	1200
1201	CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTTGGCAAAGACCAC -----+-----+-----+-----+-----+-----+-----+ GTCCCTAAAAGTATACACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG G F S Y S E E V C R C V P S Y W Q R P Q	1260

FIG. 1D



1320  
AAATGAGCTAAGATTGTACTGTGTTTTCCAGTTTCATCGATTTTCTATTATGGAAAACTGTGT  
-----+-----+-----+-----+-----+-----+-----+  
TTTACTCGATTCTTAACATGACAAAAAGGTCAAGTAGCTAAAAAGATAATACCTTTTGACACA  
M S \*  
1380  
TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCCTTGTGGGTCCATGCTAACAAAGACA  
-----+-----+-----+-----+-----+-----+-----+  
ACGGTGTCACTTGACAGACACTTGTCTCTCTGGAACACCCAGGTACGATTGTTTCTGT  
1440  
AAAGTCTGTCTTCCCTGAACCATGTGGATAACTTTACAGAAAAATGGACTGGAGCTCATCTG  
-----+-----+-----+-----+-----+-----+-----+  
TTTCAGACAGAAAGGACTTGGTACACCTATTGAAAATGTCCTTACCTGACCTCGAGTAGAC  
1500  
CAAAAGGCCCTCTTGTAAGACTGGTTTCTGCGCAATGACCAAAACAGCCAAAGATTTCCCTC  
-----+-----+-----+-----+-----+-----+-----+  
GTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCTGGTTCTTAAAGGAG  
1560  
TTGTGATTTCTTTAAAGAAATGACTATATAATTTATTTCCACTAAAAAATATTGTTTCTGC  
-----+-----+-----+-----+-----+-----+-----+  
AACACTAAAGAAATTTTCTTACTGATATATTAATAAAGGTGATTTTATACAAAGACG  
1620  
ATTCAATTTTATAGCAACAACAATGGTAAAACTCAGTGTGATCAATATTTTATATCAT  
-----+-----+-----+-----+-----+-----+-----+  
TAAGTAAAAAATATCGTTGTTGTTAAACCAATTTTGAGTGACACTAGTTATAAAAAATATAGTA  
1674  
GCAAAATATGTTTAAATAAATAATGAAAAATTTGATTTTATAAAAAA  
-----+-----+-----+-----+-----+-----+-----+  
CGTTTATACAAATTTTATTTTACTTTTAAACATAAATAATTTTATTTT

FIG. 1E



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1 CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT  
-----+-----+-----+-----+-----+-----+-----+  
61 AGATGAACATCATGACTGTACTCTACCCAGAATATTGGAAAAATGTACAAGTGTCAAGCTAAG  
-----+-----+-----+-----+-----+-----+-----+  
M T V L Y P E Y W K M Y K C Q L R  
-----+-----+-----+-----+-----+-----+-----+  
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAGAGAC  
-----+-----+-----+-----+-----+-----+-----+  
K G G W Q H N R E Q A N L N S R T E E T  
-----+-----+-----+-----+-----+-----+-----+  
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAAGTATTGATAATGAGTG  
-----+-----+-----+-----+-----+-----+-----+  
I K F A A A H Y N T E I L K S I D N E W  
-----+-----+-----+-----+-----+-----+-----+  
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT  
-----+-----+-----+-----+-----+-----+-----+  
R K T Q C M P R E V C I D V G K E F G V  
-----+-----+-----+-----+-----+-----+-----+  
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG  
-----+-----+-----+-----+-----+-----+-----+  
A T N T F F K P P C V S V Y R C G G C C  
-----+-----+-----+-----+-----+-----+-----+

FIG. 2A



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421 TGAAATTACAGTGCCTCTCTCTCAAGGCCCAACCAAGTAACAATCAGTTTGGCCAATCA  
E I T V P L S Q G P K P V T I S F A N H  
481 CACTTCCTGCCGATGCATGCTCTAAACTGGATGTTTACAGACAAGTTCATTCATTATTAG  
T S C R C M S K L D V Y R Q V H S I I R  
541 ACGTTCCTGCCAGCAACACTACCACAGTGTCTCAGGCAGCGAACAAGACCTGCCCCACCAA  
R S L P A T L P Q C Q A A N K T C P T N  
601 TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTATGTTTTCCTC  
Y M W N N H I C R C L A Q E D F M F S S  
661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAAGGAGCT  
D A G D D S T D G F H D I C G P N K E L  
721 GGATGAAGAGACCTGTGAGTGTGTCTGCAGAGCGGGCTTCGGCTGCCAGCTGTGGACC  
D E E T C Q C V C R A G L R P A S C G P

FIG. 2B



781 CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGCTGTGTAACAACTCTTCCCCAG  
H K E L D R N S C Q C V C K N K L F P S  
841 CCAATGTGGGCCAACCGAGAAATTGATGAAAAACACATGCCAGTGTGTAATAAAGAAC  
Q C G A N R E F D E N T C Q C V C K R T  
901 CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAAATGTGCCTGTGAATGTACAGAAAGTCC  
C P R N Q P L N P G K C A C E C T E S P  
961 ACAGAAATGCTTGTAAAGGAAAGAAAGTTCCACCACCAACATGCAGCTGTTACAGACG  
Q K C L L K G K K F H H Q T C S C Y R R  
1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG  
P C T N R Q K A C E P G F S Y S E E V C  
1081 TCGTTGTCCCTTCATATTGGCAAGACCAACAAATGAGCTAAGATTGTACTGTTTCCCA  
R C V P S Y W Q R P Q M S \*

FIG. 2C





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1141 GTTCATCGATTTTCTATTATGGAACACTGTGTGCCACAGTAGAACTGTCTGTGAACAGA  
-----+-----+-----+-----+-----+-----+-----+  
1201 GAGACCCTTGTGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTTCCCTGAACCATGTGGA  
-----+-----+-----+-----+-----+-----+-----+  
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAAGACTGGTTT  
-----+-----+-----+-----+-----+-----+-----+  
1321 CTGCCAATGACCCAAACAGCCCAAGATTTCCTCTTGTGATTTCCTTAAAGAAATGACTATA  
-----+-----+-----+-----+-----+-----+-----+  
1381 TAATTTATTTCCACTAAAATATTGTTTCTGCATTTCATTTTATAGCAACAACAATTGGT  
-----+-----+-----+-----+-----+-----+-----+  
1441 AAAACTCACTGTGATCAATATTTTATATCATGCAGCAAAATATGTTTAAAAATAAAATGAAAA  
-----+-----+-----+-----+-----+-----+-----+  
1501 TTGTATTATATAAAAAAAAAAAAA  
-----+-----+-----+-----+-----+-----+-----+

FIG. 2D